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1 ATGGTAAACCGGATTGTCAATACCAAGGCCCACTTAATAATCAACGGGAGTCAACATGATGTCCAATGTTCCACCTGCAGCAAAACAACACTATGGAGTCAAAA  
 33 M V N R L S I P K P N L N S T G V N M M S N V H L Q Q N N Y G V K  
 100 TCTGTGGGCCAGAGCTATGGTGTGGCCAGTCAGTGAAGGCTGGGACTAGGTGGCAATGCTCCAGTTTCCATCCCTCAACAGTCTCAGTCCCGTGAACACAG  
 66 S V G Q S Y G V G Q S V R L G L G G N A P V S I P Q Q S Q S V K Q  
 199 TTACTTCCAAGTGGGAATGGGAGGTCTTTTGGGCTAGGTGCTGAGCAGAGGCCCCAGCAGAGCCAGGTAAGTCTCCCTGCAGAGTGCACACACTCTCTTA  
 99 L L P S G N G R S F G L G A E Q R P P A A A R Y S L Q T A N T S L  
 298 CCCCCAGGCCAAGTGAAGTCTCCCTCTGTGCTCAGTCACAGGCATCTAGAGTATTAGTTCAGTCCAGTTCTAAACCTCCACCAGCCGCCACAGGCCCT  
 132 P P G Q V K S P S V S Q S Q A S R V L G Q S S S K P P A A T G P  
 165 CCTCCAAGCAACCACTGTGCCACTCAGAAGTGGGAAAATCTGTACAATCTGTAAACGAGCTTTCCCTGAGAATGTCTATAGCGTTCACTTCGAAAAAGGAG  
 198 CATAAAGCTGAGAAAGTCCAGCCGTAGCTAACTACATTAATGAAAATACACAATTTACTAGCAAAATGCCTCTACTGTAAATCGCTATTGCTCTACAGAT  
 231 H K A E K V P A V A N Y I M K I H N E T S K C L Y C N R Y L P T D  
 264 ACCCTACTCAACCATATGTTAATTCATGGTCTGTCTTGTCCGTATTGCCGTTCCACCTTCAATGATGTAGAGAAGATGGCAGCACACATTCGGAATGGTT  
 297 T L L N H M L I H G L S C P Y C R S T F N D V E K M A A H M R M V  
 330 CATATTGATGAAGAGATGGGGCTAAACCGGATCTACTTTGAGCTTTGATTGACATTTGCAACAGGGCAGTCACACCAACATTCATCTCCTGGTGACC  
 363 H I D E E M G P K T D S T L S F D L T L Q Q G S H T N I H L L V T  
 396 ACATACAACCTGAGGGATGCCCGGTGAATCAGTTGCTTACCATGCCCAATAATGCCCCAGTTCTCCAAAGCCCAACCAAAAGTTCCAGGAAAAA  
 429 T Y N L R D A P A E S V A Y H A Q N N A P V P P K P Q P K V Q E K  
 462 GCAGATGTCCCGGTTAAAGTTCACTCAGTCAGTCCCTATAAAAGATGTTGGGAAGACCCCTTTGCCCTCTTTTGCCTTTTCACTATACTAAAGGA  
 495 A D V P V K S S P Q A A V P Y K K D V G K T L C P L C F S I L K G  
 528 CCCATATCTGATGCACATCTTACGAGAAAGACCAAGATTATTCAGACAGCTTCATCCGTTGAGGAAAGATTAACCTTACAAATGTATCCAT  
 561 P I S D A L A H L R E R H Q V I Q T V H P V E K K L T Y K C I H  
 594 TGCCTTGGTGTATAGCAACATGACAGGCTCAACCATCACTCTGCTATCTGCTAGTCCAGGGGTGTTGGAAAAACCCAGAAATGGCCAGGACAAG  
 627 C L G V Y T S N M T A S T I T L H L V H C R G V G K T Q N G Q D K  
 1189 ACAACGACCTTCTCGGCTCAATCAGTCTCCAGGCTCCAGGCTGGCCCTGTGAAGCGCACGCTATGAGCAGATGGAGTTTCCACTGCTAAAAAGCGGAAGCTG  
 1288 T N A P S R L N O S P G L A P V K R T Y E Q M E F P L L K R K L  
 1387 GAGGAGGATGCTGATTCCCTAGCTGCTTTGAAGAGAGCCAGAGGCTGTGTTTGTAGCTTTAGACCCCAAGGTCATGAGATGATGATCTTATGAG  
 1486 E E D A D S P S C F E E K P E P V V L A L D P K G H E D D S Y E  
 1585 GCTAGGAAAAGCTTTCTCACAAGTACTTCAACAAACAGCCCTATCCCAAGGAGAGAAATGAGAAAGTTAGCTGCCAGTCTATGGCTATGGAAGAGT  
 1684 A R K S F L T K Y F N K Q P Y P T R R E I E K L A A S L W L W K S  
 1783 GACATTGCTCCCATTTCAAGTAAAGAGGAGAGTGTGTCGCGACTGTGAAAAGTACAAGCCCTGGTGTGCTAGTTTAAACATGAAGAATTA  
 1885 D I A S H F S N K R K K C V R D C E K Y K P G V L L G F N M K E L  
 1985 AATAAGTCAAAACACGAGATGGATTGATGCTGAGTGGCTGTTTGAATAATCAGATGAGAAAGACTCAAGAGTCAATGCTAGCAAGACTGTTGACAAA  
 2085 N K V K H E M D F D A E W L F E N H D E K D S R V N A S K T V D K  
 2185 AAGCATAACTTTGGGAAAGAAGATGATAGTCTCTCAGATAGTTTGAACATTTGGAAGAAGAAATCCAAATGGAAGCGGGAGTCTCTTTGACCTGTCTTT  
 2285 K H N L G K E D D S F S D S F E H L E E S N G S G S P F D P V F  
 2385 GAAGTTGAGCCTAAATTTCCAGTGATAATTTAGAGGAGCCTGTACCGAAGGTTATTCGGGAAGGTGCTTTGGAAATCTGAGAAAGTACACCAAAAGAG  
 2485 E V E P K I P S D N L E E P V P K V I P E G A L E S E K L D Q K E

FIG. 1A.

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1882 GAGGAGGAGGAGGAGGAGGATGGTTCAAAATATGAAACTATCCATTGACTGAGGAACCCAGCCAAATTAATGCATGATGCCTCTGATAGTGAG  
 E E E E E E E D G S K Y E T I H L T E E P A K L M H D A S D S E 660  
 1981 GTAGACCAAGATGATGTAGTTGAGTGGAAGATGGTCTTACCATCTGAGAGTGGCCCTGGTTCCCAACAAATCTCAGACTTTGAGGATAAATACATGT  
 V D Q D D V V E W K D G A S P S E S G P G S Q Q I S D F E D N T C 693  
 2080 GAAATGAAACCAAGAACCTGGTCTGATGAGTCTTCCACAGATGAAGATGCAAGGAGCAGTAAGCCAGTGTGCCAAAAAAGGCTACAGTGCAAGATGAC  
 E M K P G T W S D E S S Q S E D A R S S K P A A K K K A T V Q D D 726  
 2179 ACAGAGCAGTTAAATGGAAGAATAGTTCCCTATGGAAGTTGAAGGGTTTGGTCCCAAGGACCAGTACAGTGGGAAATGCATCTGAGAAATGCAGAG  
 T E Q L K W K N S S Y G K V E G F W S K D Q S Q W E N A S E N A E 759  
 2278 CGCTTACCAACCCACAGATTGAGTGGCAGAAATAGCACAATTGACAGTGAGGACGGGAGCAGTTTGACAGCATGACTGACGGAGTTGCTGATCCCATG  
 R L P N P Q I E W Q N S T I D S E D G E Q F D S M T D G V A D P M 792  
 2377 CATGGCAGCTTAAGTGGAGTGAAGCTGAGCAGCCAGCAAGCCTGA  
 H G S L T G V K L S S Q Q A \* 806

Single Underline - homologies to HSP60 of ADNP

Dotted Underline - homologies to PIF1 of ADNP

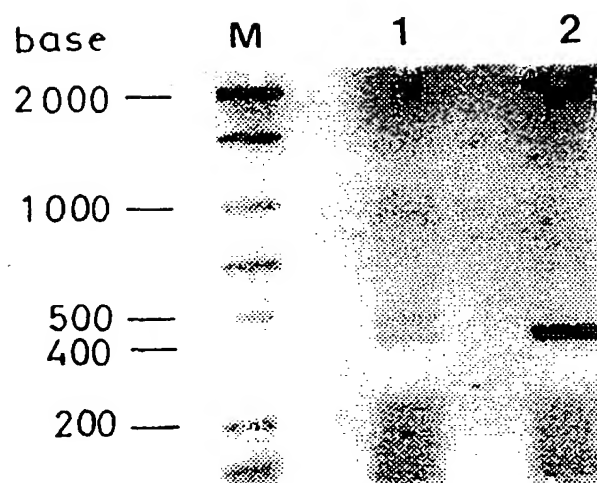
Double Underline - Glycosylation site (amino acid no. 96-98, 183-185, 371-373, 404-406, 554-556, 584-586, 734-736, 753-755, 770-772)

Bold + Italic - represents two motifs:

1. Glutaredoxin active site (amino acid no. 211-221)
2. Zinc finger C2h2 type, domain (amino acid no. 211-232)

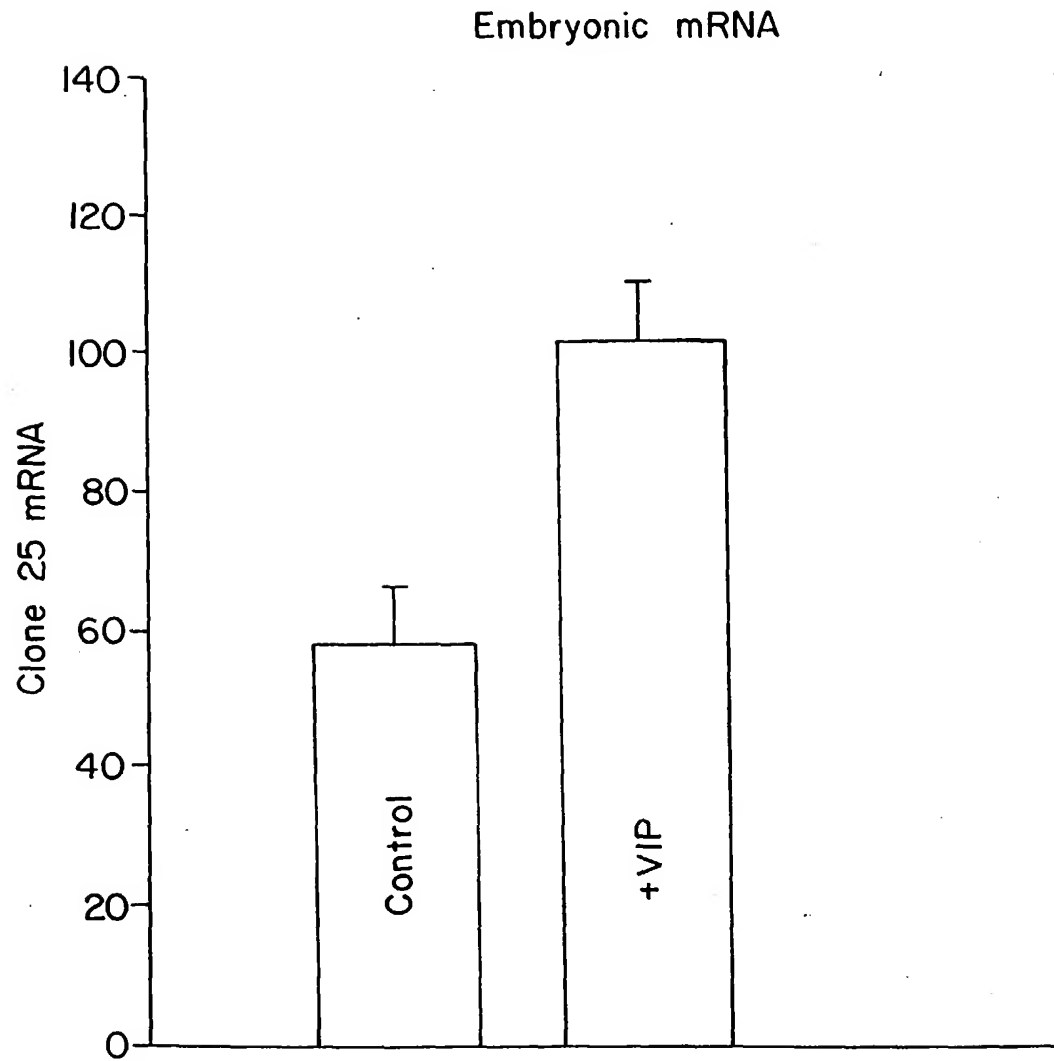
FIG. 1B.

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**FIG. 2.**

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**FIG. 3**

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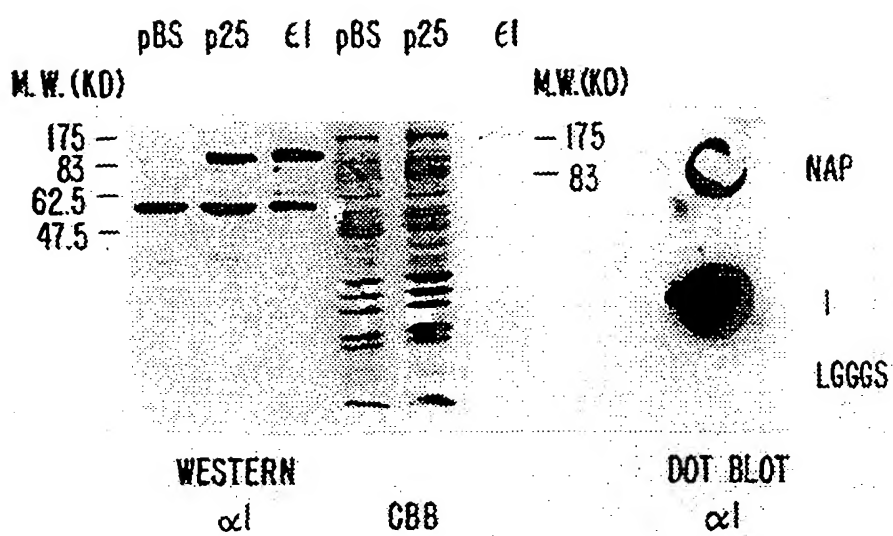


FIG. 4A.

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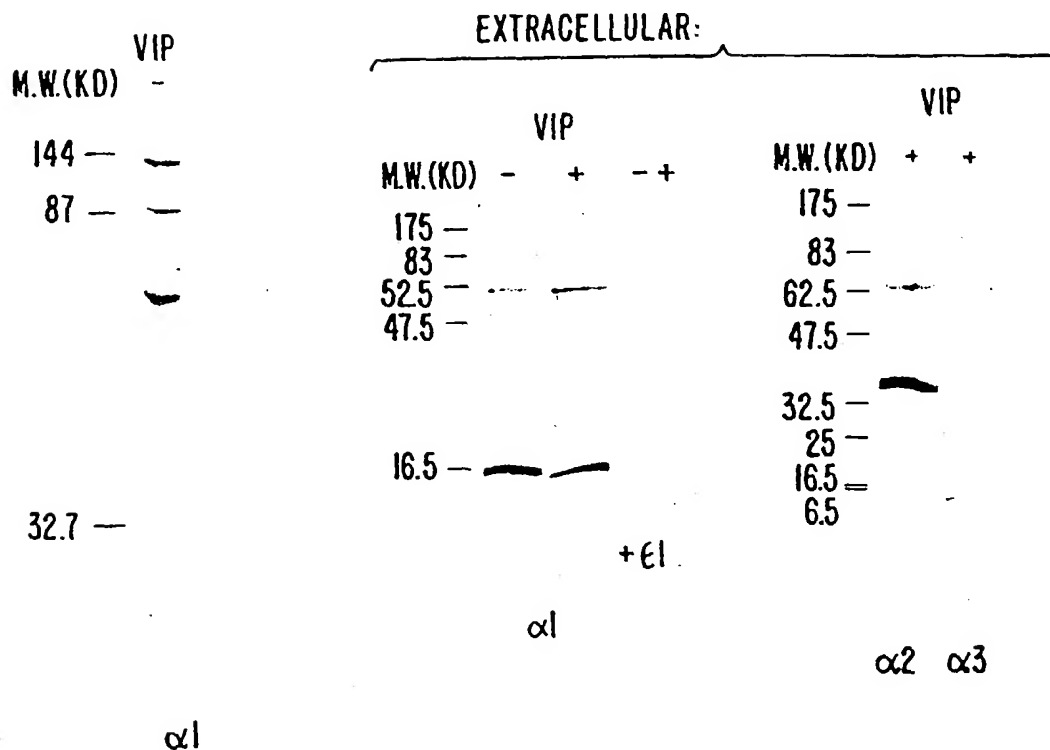
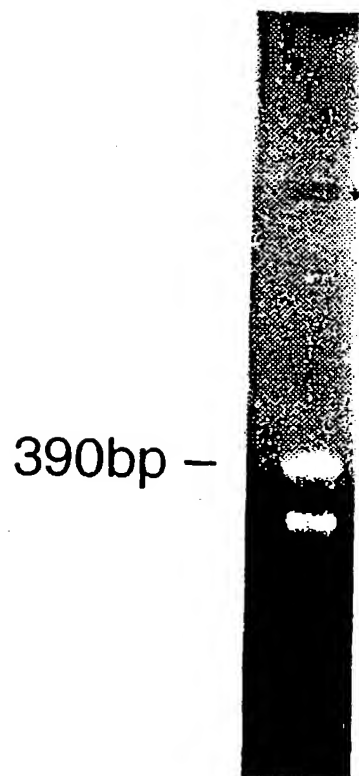


FIG. 4B.

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**Neuroblastoma (NMB)**

*FIG. 5A.*

SENSE

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1 CATTGGGCGG ACGTCGCATG CTCCCGGCCG CCATGGCCGC GGGATTACCT  
51 GCAGCAAAAC AACTATGGAG TCAAATCTGT AGGCCAGGGT TACAGTGTTC  
101 GTCAGTCAAT GAGACTGGGT CTAGGTGGCA ACGCACCAGT TTCCATTCTT  
151 CAACAATCTC AGTCTGTAAA GCAGTTACTT CCAAGTGGAA ACGGAAGGTC  
201 TTATGGGCTT GGGTCAGAGC AGAGGTCCCA GGCACCAGCA AGATACTCCC  
251 TGCAGTCTGC TAATGCCTCT TCTCTCTCAT CGGGCCAGTT AAAGTCTCTT  
301 TCCCTCTCTC AGTCACAGGC ATCCAGAGTG TTAGGTCAGT CCAGTTCCAA  
351 ACCTGCTGCA GCTGCCACAG GCCCTCCCCC AGGTAACACT TCCTCAACTC  
401 AAAAGTGGAA AATATGTACA ATCTGTAACG AGCAATCACT AGTGCGGCCG  
451 CCTGCAGGTC GACCATATGG GAGAGCTCCC AACGCGTTGG ATGCATAGCT  
501 TGAGTATTCT ATAGTGTAC CTAATAGCT TGGCGTAATC ATGGTCATAG  
551 CTGTTTCTCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG  
601 AACCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA ATGAGCTAAC  
651 TCACATTAAT TGC GTTGC GC TCACTGCCCC CTTTCCAATC NGGAAACTGT  
701 CGTGCCAACT GCATTAATGA ATCGGCCAAC GCGCGGGGAA AAGCGGTTTG  
751 CGTATTGGGC GCTCTTCCGC TTCCTCGCTC AATGAATCCC TGCGCTCNGT  
801 CCTTCCGNTG CGGNNAACGG TATCACTCAC TCNAATT

ANTISENSE

1 ATNNATATCA AGCTATGCAT CCAACGCGTT GGGAGCTCTC CCATATGGTC  
51 GACCTGCAGG CGGCCGCACT AGTGATTCT CGTTACAGAT TGTAATATT PRIMER 44  
101 TTCCACTTTT GAGTTGAGGA AGTGTTACCT GGGGAGGGC CTGTGGCAGC  
151 TGCAGCAGGT TTGGAAGTGG ACTGACCTAA CACTCTGGAT GCCTGTGACT  
201 GAGAGAGGGA AGGAGACTTT AACTGGCCCG ATGAGAGAGA AGAGGCATTA  
251 GCAGACTGCA GGGAGTATCT TGCTGGTGCC TGGGACCTCT GCTCTGACCC  
301 AAGCCCATAA GACCTTCCGT TTCCACTTGG AAGTAACTGC TTTACAGACT  
351 GAGATTGTTG AGGAATGGAA ACTGGTGCGT TGCCACCTAG ACCCAGTCTC  
401 ATTGACTGAC CAACACTGTA ACCCTGGCCT ACAGATTTGA CTCATAGTT - PRIMER 105  
451 GTTTTGCTGC AGGTAAATCCC GCGGCCATGG CGGCCGGGAG CATGCGACGT

FIG. 5B-1.



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501 CGGGCCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG  
551 TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCCC  
601 CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG CGTTAATAAC GAAGAAGCCC  
651 GCACCGATCG CCCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGACG  
701 CGCCTGTTAG CGCGCATTAA ACCCCGCGGG TGTTGTGGTT ACGCCGCAGC  
751 GTGACCGCTA CACTTGCCAC CCCCTAACGC CCGCTCCTTT CCCTTTCTTC  
801 CTTCCCTTTCT CGCCACGTCC CCCGNTTTC CCGTCCAACCT CTAAATCGGT

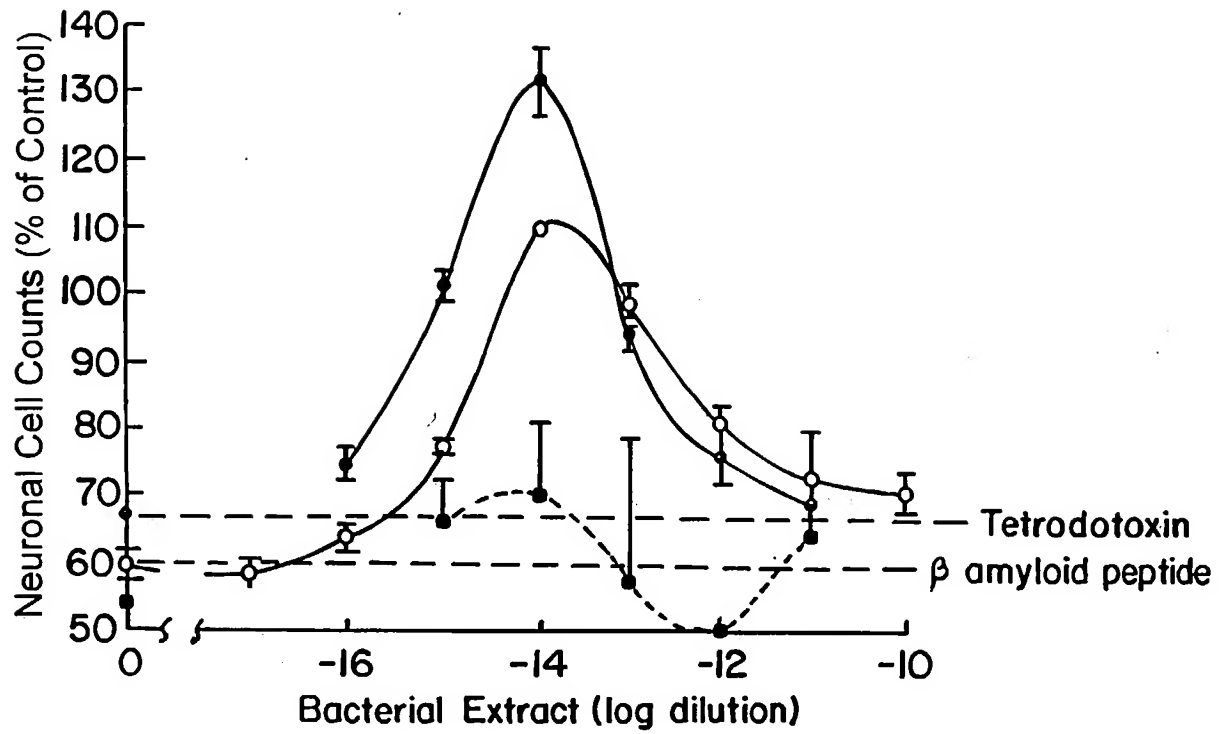
*FIG. 5B-2.*

**FIG. 5C-1.**

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FIG. 5C-2.

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**FIG. 6A**

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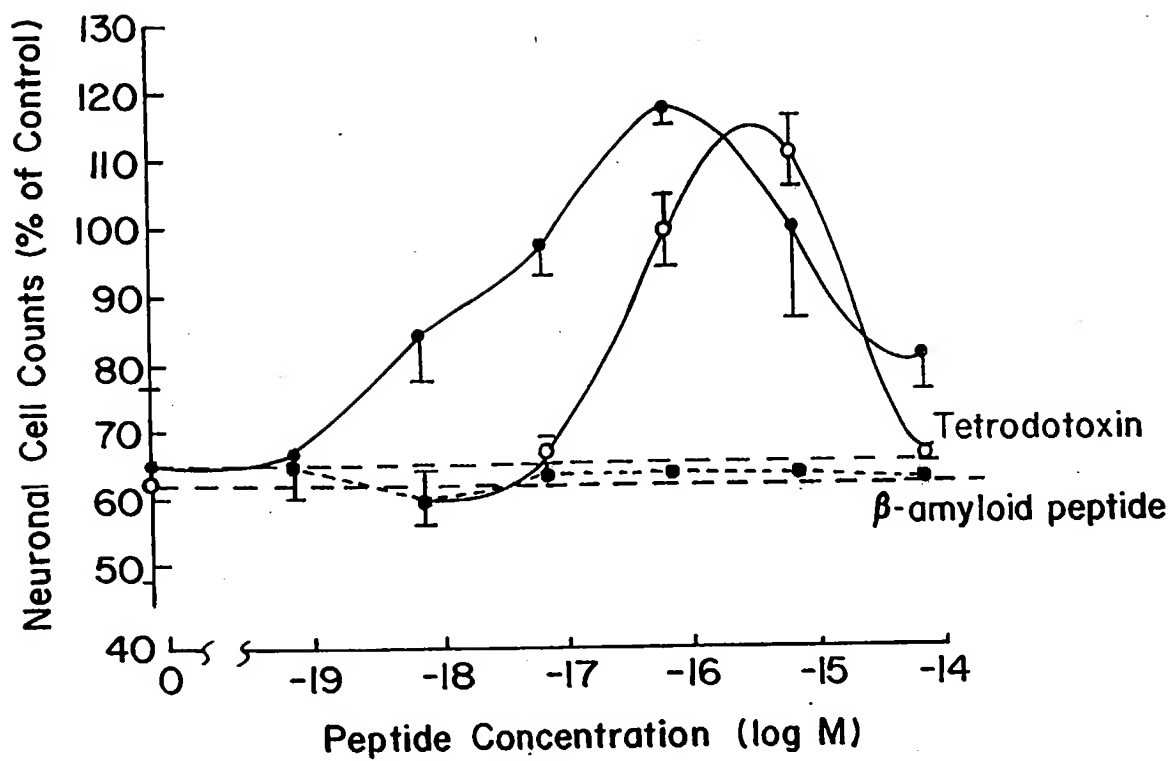


FIG. 6B

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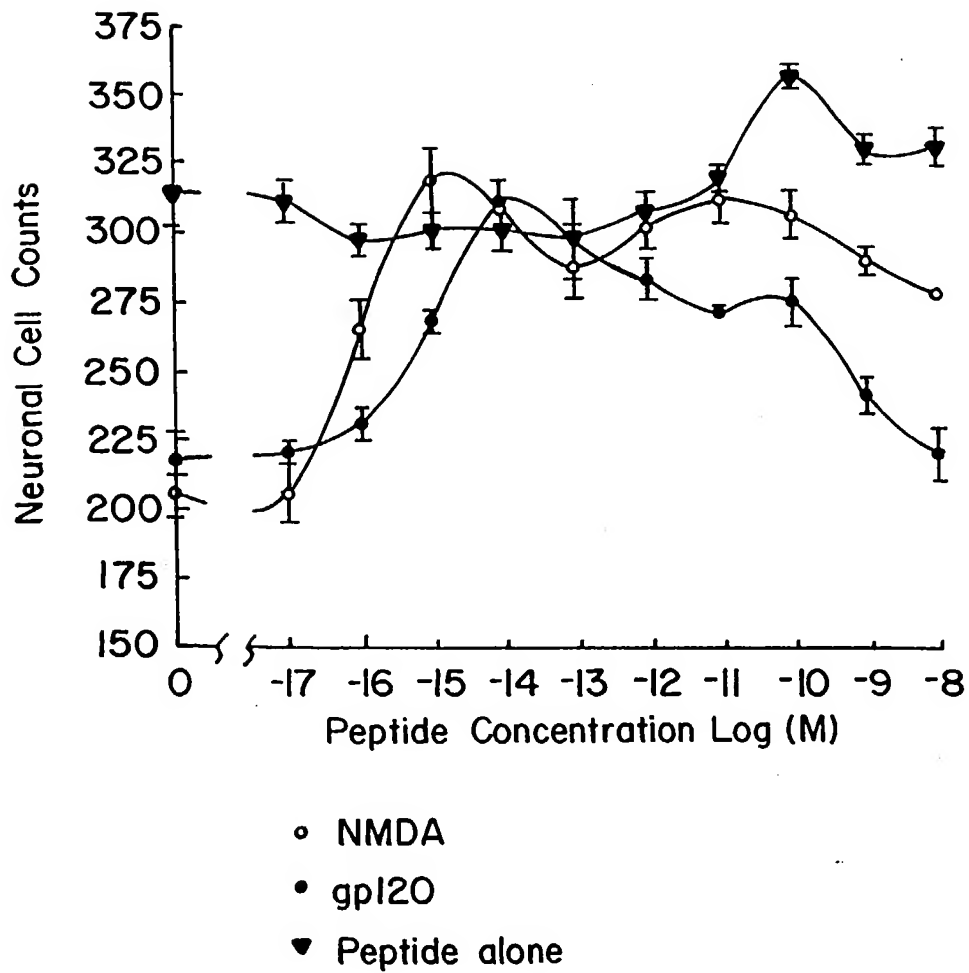


FIG. 6C

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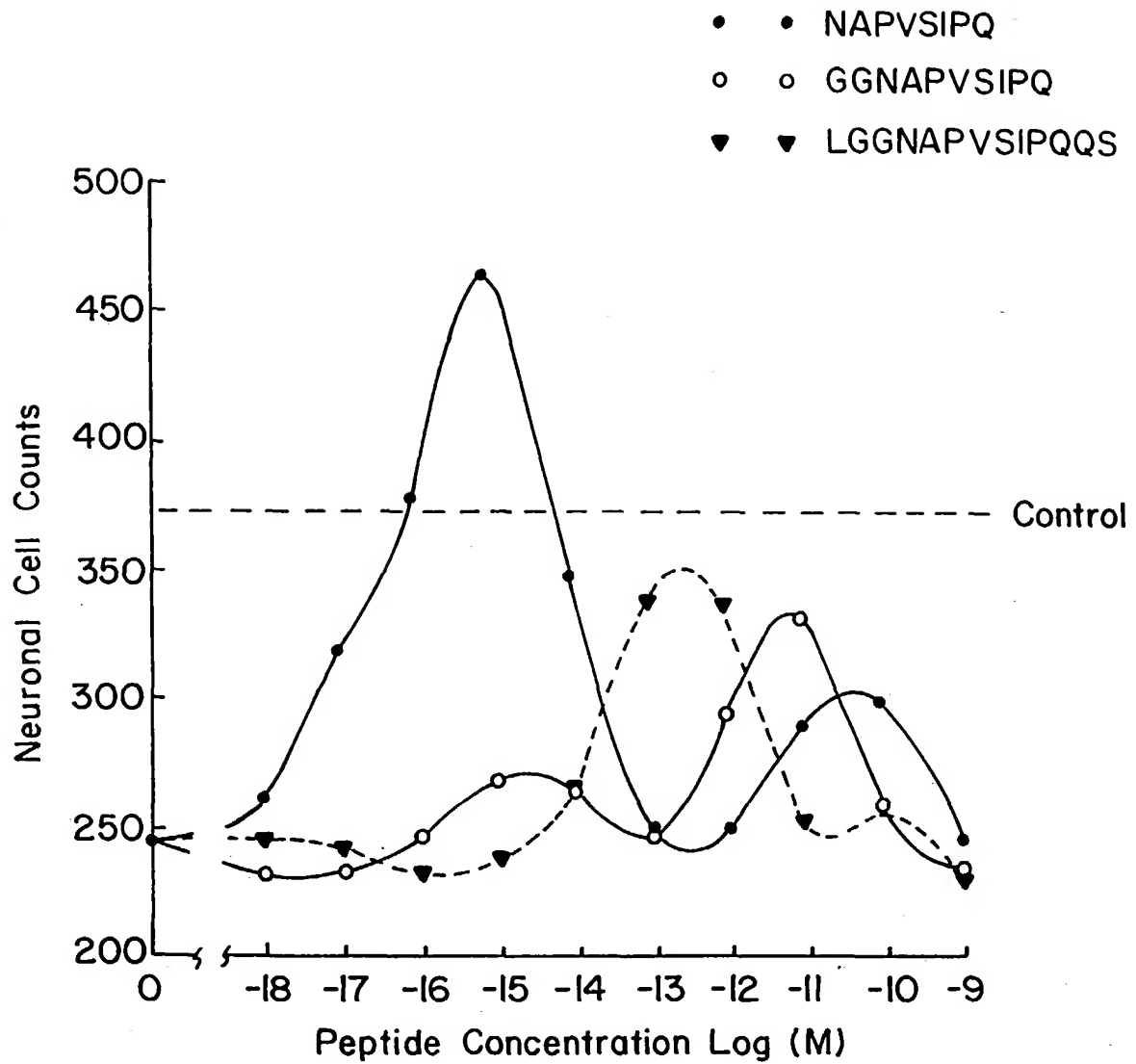


FIG. 7A

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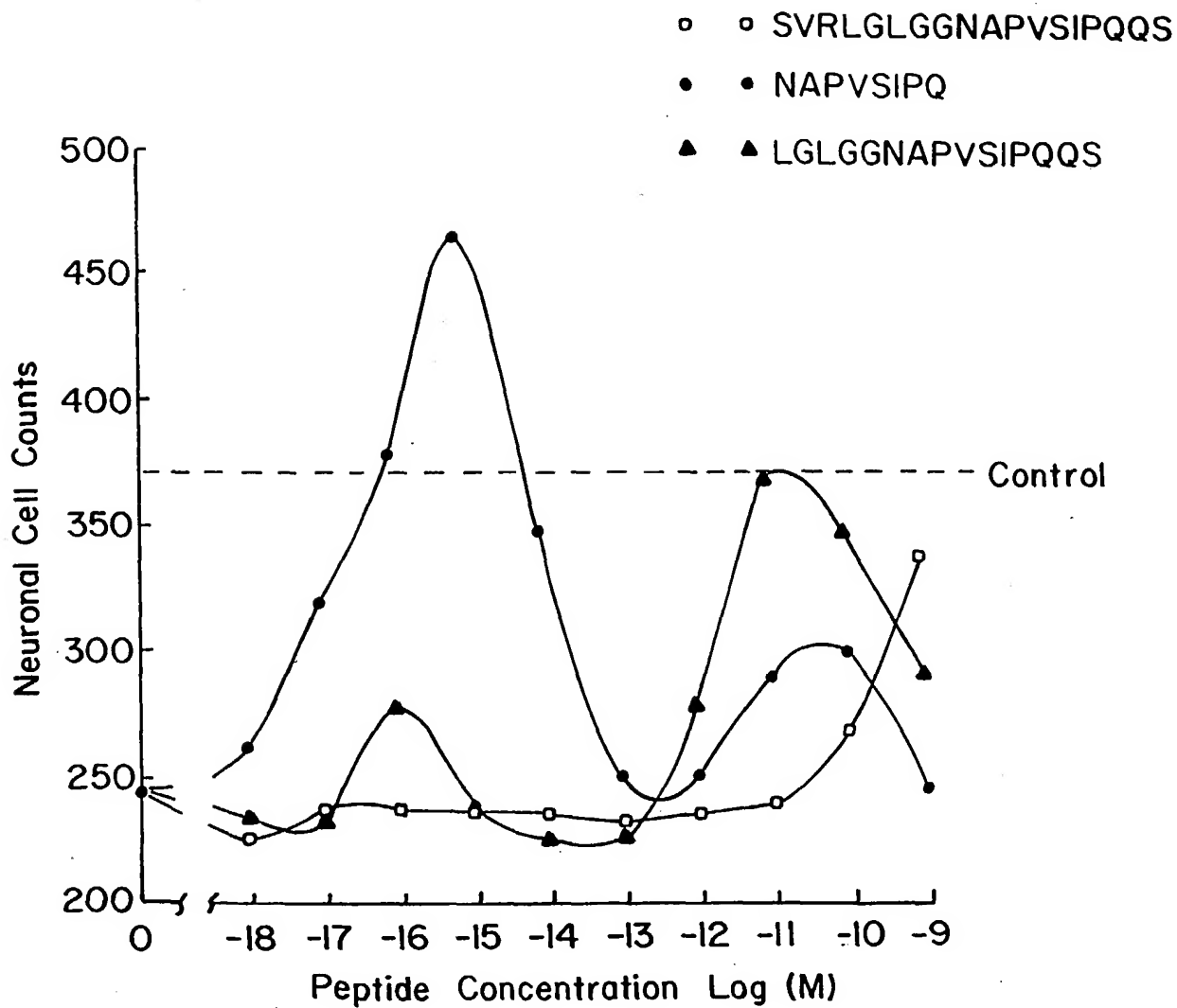


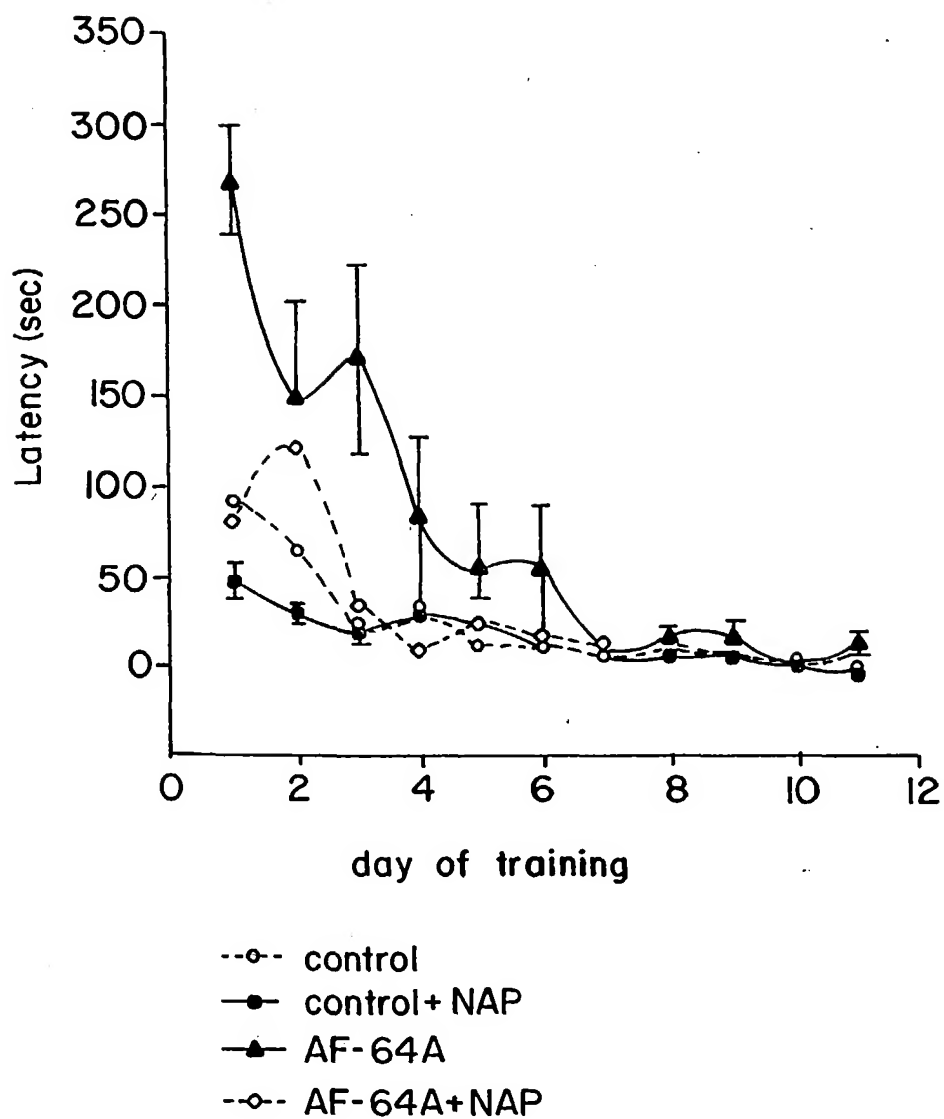
FIG. 7B



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# The effect of NAPVSIPQ(NAP) on learning and memory



**FIG. 8**

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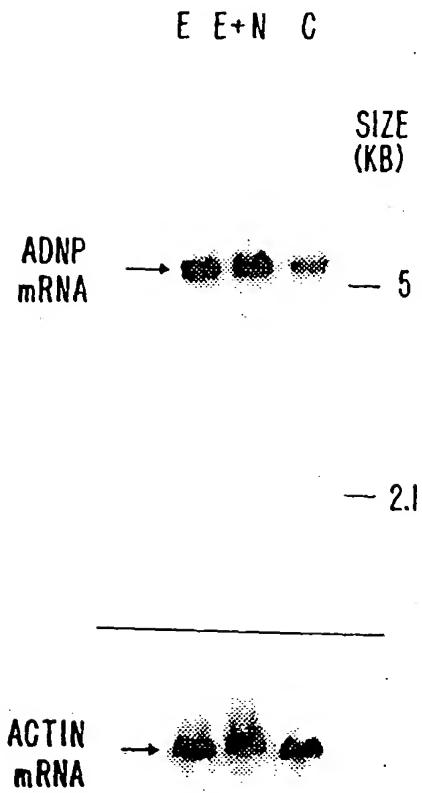


FIG. 9.

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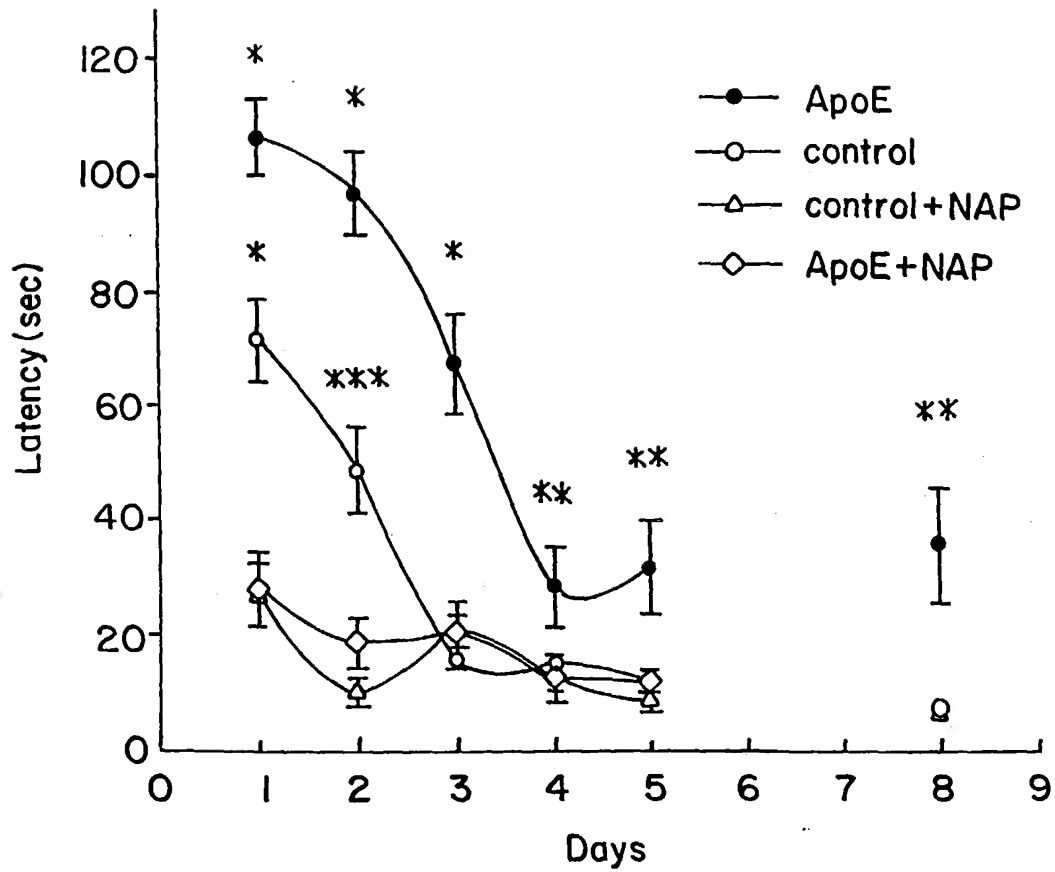


FIG. 10

**FIG. 11A.**

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E E P V P K V I P E G A L E S E K L D Q K E E E E E D G S 660  
1981 AAATATGAACATATCCATTGACTGAGGAACCCAGCCAAATTAATGATGATGCTCTGATAGTGAGGTAGACCAAGATGATGTAGTTGAGTGGAAAGAT  
K Y E T I H L T E E P A K L M H D A S D S E V D Q D D V V E W K D 693  
2080 GGTGCTTCACCATCTGAGAGTGGGCTGGTTCCCAACAATCTCAGACTTTGAGGATAATACATGTGAAATGAAACCCAGGAACCTGGTCTGATGAGTCT  
G A S P S E S G P G S Q Q I S D F E D N T C E M K P G T W S D E S 726  
2179 TCCAGAGTGAAGATGCAAGGAGCAGTAAGCCAGTGCCTCCAAAAAGGCTACAGTGCAAGATGACACAGAGCAGTTAAATGGAAGATAAGTTCTTAT  
S Q S E D A R S S K P A A K K A T V Q D D T E Q L K W K N S S Y 759  
2278 GGAAAGTTGAAGGGTTTGTGTCACAGGACCCAGTCCAGTGGGAAATGCAATGAGATGAGAGCGCTTACCAACCCACAGATTGAGTGGCAGAAT  
G K V E G F W S K D Q S Q W E N A S E N A E R L P N P Q I E W Q N 792  
2377 AGCACAATTGACAGTGGGACGGGAGCAGCTTTGACAGCATGACTGACGGAGTTGCTGATCCCATGCGAGCTTAACCTGGAGTGAAGCTGAGCAGC  
S T I D S E D G E Q F D S M T D G V A D P M H G S L T G V K L S S 825  
2476 CAGCAAGCCTGA  
Q Q A \*

Single Underline - homologues to HSP60 of ADNP

Double Underline - Glycosylation site (amino acid no. 118-120, 205-207, 393-395, 426-428, 576-578, 606-608, 756-758,  
775-777, 792-794)

Bold + Italic - represents two motifs:

1. Glutaredoxin active site (amino acid no. 233-243)
2. Zinc finger C2h2 type, domain (amino acid no. 233-254)

Bold - potential proteolytic cleavage sites.

Bold + Underline - putative signal peptide

FIG. 11B.

**FIG. 12A.**

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1927 TCTGAGGAGAGCTAGACCAAAAGAGGATGGTTCAAAATACGAAACTATTTCATTGACTGAGGAACCAACCAACTAATGCACAATGCAATCTGATAGT  
S E K L D Q K E D G S K Y E T I H L T E E P T K L M H N A S D S 675  
2026 GAGGTTGACCAAGACGATGTTGTTGAGTGGAAGACGGTGCTTCTCCATCTGAGAGTGGGCTGGATCCCAACAAGTGTGAGACTTTGAGGACATACC  
E V D Q D D V E W K D G A S P S E S G P G S Q Q V S D F E D N T 708  
2125 TCCGAATGAACCAAGACCTGGTCTGACGAGTCTTCCCAAGCGAAGATGCAAGGAGCAGTAAGCCAGCTGCCAAAAAAGGCTTACCATGCCAAGG  
C E M K P G T W S D E S S Q S E D A R S S K P A A K K K G Y H A R 741  
2224 TGA \*

Single underline - homologies to hsp60 of ADNP.

Double underline - Glycosilation sites.

Bold + Double underline -

1. Zinc finger C2h2 type, domains.
2. Glutaredoxin active site (amino acid no. 234-238)

Bold - potential proteolic cleavage site.

H3

FIG. 12B.

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H7 clone

AAAACGAGGACTATCGGACAAAACCTTTCTGCTGCGCGCTTGTCCTCAAAATTTCTTCTCTGCTTACAAAAGTCATTTCCGCAATGTCCAT  
AGTGAAGACTTTTGAATAAGGATTCCTTAATTGCCCCCTACTGTACCTTCAATGCGACAAAAGACTTTGGAAACACACATTAAATAATATTTTCATGCT  
CCGAACGCCAGCGCAACCAAGTAGCAGCTTCAGCACCTTTCAAAAGATAAAACCAAAAATGATGGCCTTAAACTTAAGCAGGCTGACAGTGTAGAGCAAGCT  
GTTTATTCTGTAAAGTGCACCTTACCGAGATCCTCTTTATGAATAAGTTAGGAAGCAGCATTATACAGGGAACATTTTCAGCATGTGGCAGCACCTTAC  
ATAGCAAGGCGAGGAGAAAATCACTCAATGGGGCAGTCCCCCTTAGGCTCGAATGCCCCGAGAGAGAGTAGTATTCTACTGCAAGCGATGCCCTTTTCATG  
M  
CCAAAGTCCTATGAAGCTTTGGTACAGCATGTCTATCGAAGACCATTGAACGTATAGGCTATCAGGTCACTGCCATGATTTGGGCACACAAAATGTAGTGGTT  
P K S Y E A L V Q H V I E D H E R I G Y Q V T A M I G H T N V V  
54 CCGGATCCAAACCTTGATGCTAATGCTCCCAACCTCAAGACAAAGAGCAGTGGGACTCCCAACCAAGGATCGGTTCCCTTCTCTGGAAATGTC  
P R S K P L M L I A P K P Q D K K S M G L P P R I G S L A S G N V  
45 CGGTCTTTACCATCAGCAGAGATGGTGAATCGACTCTCAATACCAAGCCTAACTTAAATTTCTACAGGAGTCAACATGATGCCAGTGTTCATCTGCAG  
R S L P S Q Q M V N R L S I P K P N L N S T G V N M S S V H L Q  
144 CAGAACAACTATGGAGTCAAAATCTGTAGGCCAGGTTACAGTGTGGTCAATGAGACTGGGTCTAGGTGGCAACGCACACAGTTTCCATTCCCTCAA  
Q N N Y G V K S V G Q G Y S V G Q S M R L G L G G N A P V S I P Q  
243 CAATCTCAGTCTGTAAAGCAGTACTTCAAGTGGAAACGGAAGTCTTATGGCTTGGTCAAGCAGAGAGGTCCCAGGCACCAAGATACTCCCTG  
Q S Q S V K Q L L P S G N G R S Y G L G S E Q R S Q A P A R Y S L  
342 CAGTCTGTAATGCTTCTCTCTCATCGGGCCAGTTAAAGTCTCTCCCTCTCTCAGTCACAGGCATCCAGAGTGTAGGTCCAGTCCAGTTCCTCAA  
Q S A N A S L S S G Q L K S P S L S Q S Q A S R V L G Q S S K  
441 CCTGCTGAGCTGCCACAGGCCCTCCCCAGGTAACTCTCTCAACTCAAAAGTGGAAATATGTACAATCTGTAAATGAGCTTTTCTCTGAAATGTC  
P A A A T G P P P G N T S S T Q K W K I C T I C N E L F P E N V  
540 TATAGTGTGCACCTTCGAAAAAGAACATAAAGCTGAGAAAGTCCAGCAGTAGCCAACTACATTATGAAAAATACACAATTTTACTAGCAAAATGCCTCTAC  
Y S V H F E K E H K A E K V P A V A N Y I M K I H N F T S K C L Y  
639 TGTAAATCGCTATTTACCCACAGATACTGTCTCAACCATATGTTAATTCATGCTGTCTGTCCATATGCGGTCAACTTTCAATGATGTGGAAGAAG  
C N R Y L P T D T L L N H M L I H G L S C P Y C R S T F N D V E K  
738 ATGGCCGCACACATGGGATGGTTACATTGATGAAGAGATGGGACCTAAACACAGATTCTACTTTGATTTTGACATTCAGCAGGAGGTGATGCAC  
M A A H M R M V H I D E E M G P K T D S T L S F D L T L Q Q G S H  
837 ACTAACATCCATCTCTGTAAAGGAGAGATATCCCTGTAAAGGTTTCAAGTGCAGTGCCTTAAAGGATGTGGGAAAAACCTTTGTCTCT  
T N I H L L V T T Y N L R D A P A E S V A Y H A Q N N P P P P K  
936 CCACAGCCAAAGGTTTCAGGAAAGGAGAGATATCCCTGTAAAGGTTTCAAGTGCAGTGCCTTAAAGGATGTGGGAAAAACCTTTGTCTCT  
P Q P K V Q E K A D I P V K S S P Q A A V P Y K K D V G K T L C P  
1035 CTTTGTCTTTCAATCCATAAAGGAGCCCATATCTGATGCACTTGCACATCACTTACGAGAGAGGCACCAAGTTATTCAGACGGTTCATCCAGTTGAGAAA  
L C F S I L K G P I S D A L A H L R E R H Q V I Q T V H P V E K  
1134 AAGCTCACCTACAAATGTATCCATTTGCTGTTGATATACCAAGCAACATGACCGCTCAACTCATCTGCTGATCTAGTTTCACTGCGGGCGGTGGA  
K L T Y K C I H C L G V Y T S N M T A S T I T L H L V H C R G V G  
1233 AAGACCCAAATGGCCAGGATAGACAAATGACCCCTCTCGGCTTAATCAGTCTCCAAAGTCTGCGCACCTGTGAAGCGCACTTACGAGCAAAATGGAATTT

FIG. 13A.



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K T Q N G Q D K K T N A P S R L N Q S P S L A P V K R T Y E Q M E F  
1332 CCCTTACTGAAAAACGAAAGTTAGATGATAGTAGTATTCACCCAGCTTCTTTGAAGAGAGAGCCTGAAGAGCCTGTTGTTTGTAGCTTTAGACCCCAAG  
P L L K K R K L D D S D S P S F F E E K P E E P V V L A L D P K  
1431 GGTATGAAGATGATTCCTATGAAGCCAGGAAAGCTTTCTTAACAAGATATTTCAACAACAGCCCTATCCACAGGAGAGAAAATTTGAGAAGCTAGCA  
G H E D D S Y E A R K S F L T K Y F N K Q P Y P T R R E I E K L A  
1530 GCCAGTTTATGGTATGAAGAGTGACATCGCTTCCCATTTTAGTAACAAGGAAGAAGTGTGTCGCTGATTTGTGAAAAGTACAAGCCTGGCGTGTG  
A S L W L W K S D I A S H F S N K R K K C V R D C E K Y K P G V L  
1629 CTGGGGTTTAACATGAAGAATTAATAAAGTCAAGCATGAGATGGATTTTGATGCTGAGTGGCTATTTGAAAATCATGATGAGAAGGATTCAGAGTC  
L G F N M K E L N K V K H E M D F D A E W L F E N H D E K D S R V  
1728 AATGCTAGTAAGACTGTCACAAAAGCTCAACCTTGGGAAGGAAGATGACAGTTCCTCAGACAGTTCCTGAAAATTTGGAAGAAGAAATCCAATGAAAGT  
N A S K T A D K K L N L G K E D D S S S D S F E N L E E S N E S  
1827 GGTAGCCCTTTTGACCCTGTTTGAAGTTGAACCTAAAATCTTAACGATTAACCCAGAGAACAATGTAAGTAATTCCTGAGGATGCTTCAGAA  
G S P F D P V F E V E P K I S N D N P E E H V L K V I P E D A S E  
1926 TCTGAGGAGAGCTAGACCAAAAAGAGATGGTTCAAAATACGAAACTATTCATTTGACTGAGGAACCAACCAAACTAATGCACAATGCATCTGATAGT  
S E E K L D Q K E D G S K Y E T I H L T E E P T K L M H N A S D S  
2025 GAGGTTGACCAAGACGATGTTGTTGAGTGGAAAGACGGTGTCTTCCATCTGAGAGTGGCCTGGATCCCAAGTGTGAGACTTTTGAGGACATATACC  
E V D Q D D V V E W K D G A S P S E S G P G S Q Q V S D F E D N T  
2124 TGCAGAAATGAACAGGAACCTGGTCTGACAGTCTTCCAAAGCGAAGATGCAAGGAGCAGTAAGCCAGCTGCCAAAAAGGCTACCATGCAAGGT  
C E M K P G T W S D E S S Q S E D A R S S K P A A K K A T M Q G  
2223 GACAGAGAGCAGTTGAAGAATAAGTTCTCTATGGAAAGTTGAAGGTTTGGTCTAAGGACCAGTCACAGTGAAGAATGCATCTGAGATGAT  
D R E Q L K W K N S S Y G K V E G F W S K D Q S Q W K N A S E N D  
2322 GAGCGCTTATCTAACCCAGATTTAGTGGCAAGATAGCACAAATGACAGTGGGAGGATGGGACAGTTTGACACATGACTGATGGAGTAGCTGAGCCC  
E R L S N P Q I E W Q N S T I D S E D G E Q F D N M T D G V A E P  
2421 ATGCATGGCAGCTTAGCCGGAGTTAAACTGAGCAGCCCAACAGGCTTAAGTGCCAGGTTCCCTGGCATTTGGTGACATGCTGCAGCCTGGAACCTCTGATCT  
M H G S L A G V K L S S Q Q A\*  
2520 CCAGTGTGACTGCAAGAGCTGTCTTCTCACTGGTACTGCCTTGTGAGTACTGGTGGACTGTGGGGCATGTGGCCGCTGCAGTTCCAGTGGTTATTTCTA  
2619 AGTCTATGACAGGACAGGCTGTTCTTGCTTCAGAACCTTCTCTGACAGACACGGTAACTAAATGTGAAAAACCAATAAGCTGGTGACTCATGAATACAC  
2718 ACAGGAAAAAGCAGAGGTTTATTTTATCTGCCCTTTTCAACATTTCTTCCCTCTGTGAAATGATTGGTGCAGATGTCTTTTGAGAAGTGTAAACTAATTC  
2817 ACATGGTAGTAGGCCCACATACAAGCTACCAGTCTAATGTGTATAGTAGACTTTGGGAAAAGCGATTTTTTTTCATGTATTCTGAAATAGTTG  
2916 AAATGTATATTTTACAGTCTTTTAGACCTATTCAAGTAGTGCTCATGATCCTGTTACTGTGTGCCCATCATAGATTTCTTTTTTAGTGTGGCCCTTG  
3015 CTGTGTAATAAACGCTCTATCTAGTTTACCTAGCAAAAGCTCAAAAACCTGGCTAGTATGGACTTTTGGACAGACTAGTTTTTGGCACATAACCTTGTA  
3114 CAATCTTGCAACAGAGGCCAGCCACGTAAGATATATATCTGGACTCTCTTGGATTATAGGATTTTCTTGGTCTGAATATCCTTGACATTACAGCTGTCT

FIG. 13B.

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3213 AAAACAAAAA CTGGTATTTCCAGATCTGTTTTCTGAAATCTTTTAAGCTAAAAATCACATGCAAGAATTGACTTTGCAGCTACTAATTTTGACACCTTTT  
3312 AGATCTGTATAAAAAGTGTGTTGAAGCAGCAAAACCAATGAGTGTGCTGCATTTTGGATAATTTAGTTTATCTTTTAGTTCAACACCATCATGGTGGAT  
3411 TCATTTATACCATCTAATATATGACACACTGTTGTAGTATGTATAATTTTGTGATCTTTTATTTTCCCTTTGTATTTCATTTTAAAGCATCTAAATATAATTG  
3510 CTGTATTGTGCTTAATGTAAAAAATAAAAAA

Bold: Putative initiator methionine

**initiator methionine** in the mouse sequence (numbers of nucleic acids and amino acids is according to the mouse sequence).

**initiator methionine**: polymorphic site

FIG. 13C.

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1 AATTGTTGGG TGATGAGAAA GAGAGCTGTT TGCCTTCCGT GTTGGTCATC  
51 AAGGTCTGCG TGCATTGCAA CAGTGTCAAC TGTGAGTTCC TGTGTCTGAA  
101 GCCGAGAAGA TCCACAAAAT GAGGCTTTTC CATAGTTGGT TTGTGTTTTT  
151 AACAAAGAAAA TGGAGAGGCT TTTTGTTTGT TTTTGTTTTT GTTTTTTTGC  
201 CTCTGACTTC TCTCTGAAAC CAGCCAACAA GTACAACTAG CAATTTTAA  
251 AGATTTAGCA AGAACTTGCA CTGAGTTTTC ATTTACAGGA GCACAAATAA  
301 AAATATTTGA TTCAAAAATG CATCTGAGTT CTTTAAATTT TTCCTGCAGG  
351 AGAAACCTCT AAAAGTCATT GCCTTGAGA GTTCTGGGA ATGCCTGGGG  
401 GAGGAGCCTG GAACTTGTA CTGCTTGCCT TGAGTGGCCT TCTCACTCTG  
451 GTTCTGTTC TGTTTGTGTT CGTTTGTGTT TT

FIG. 14.

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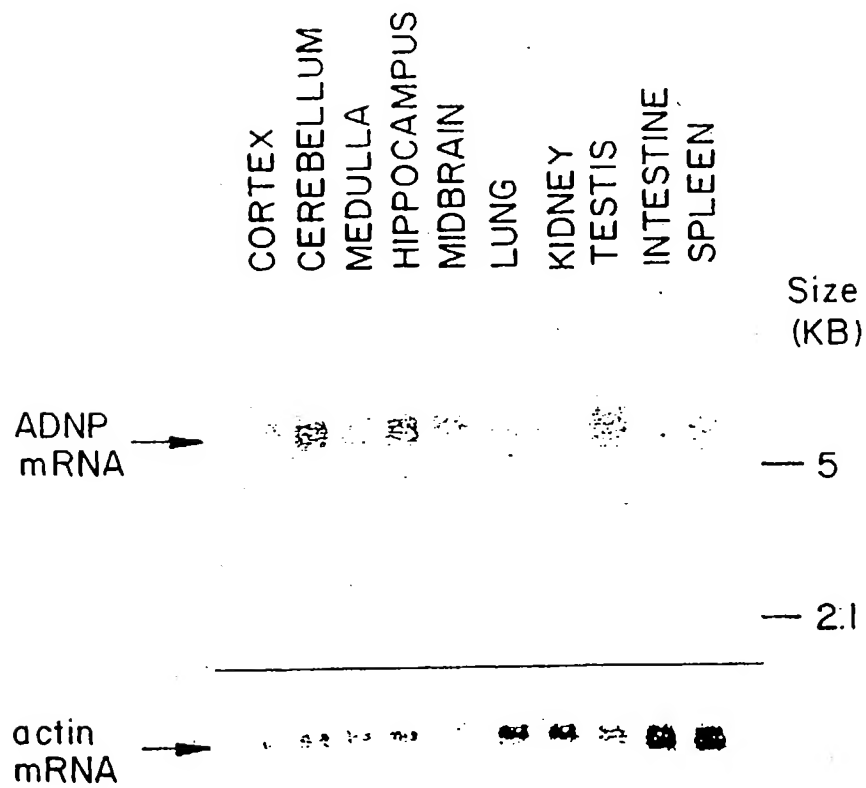


FIG. 15.

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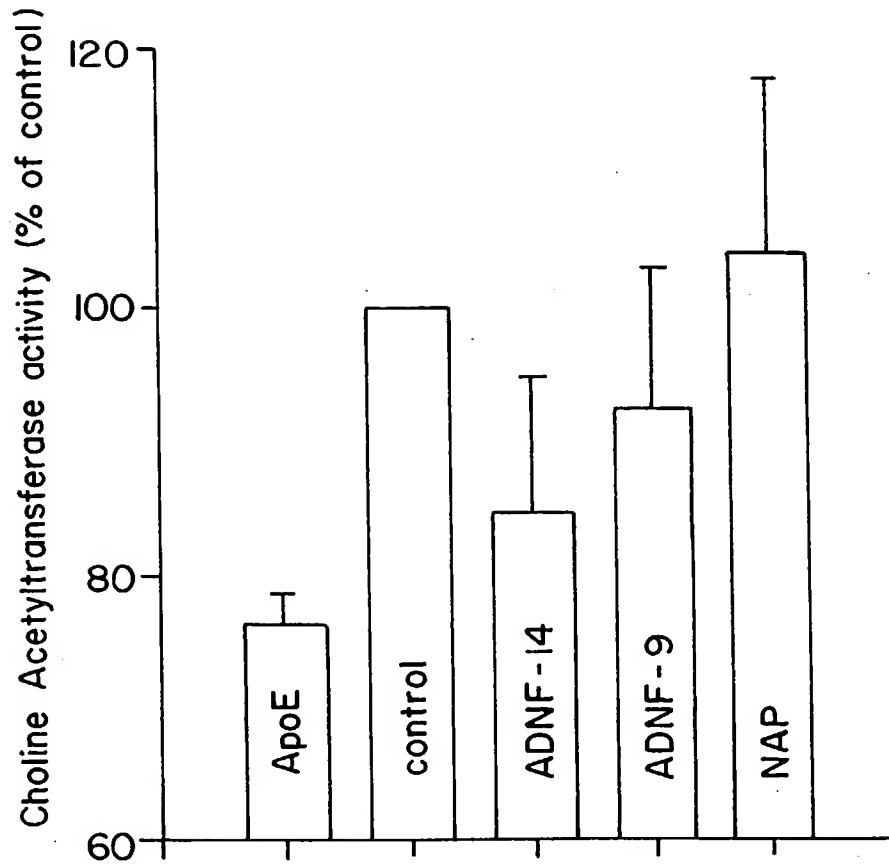


FIG. 16

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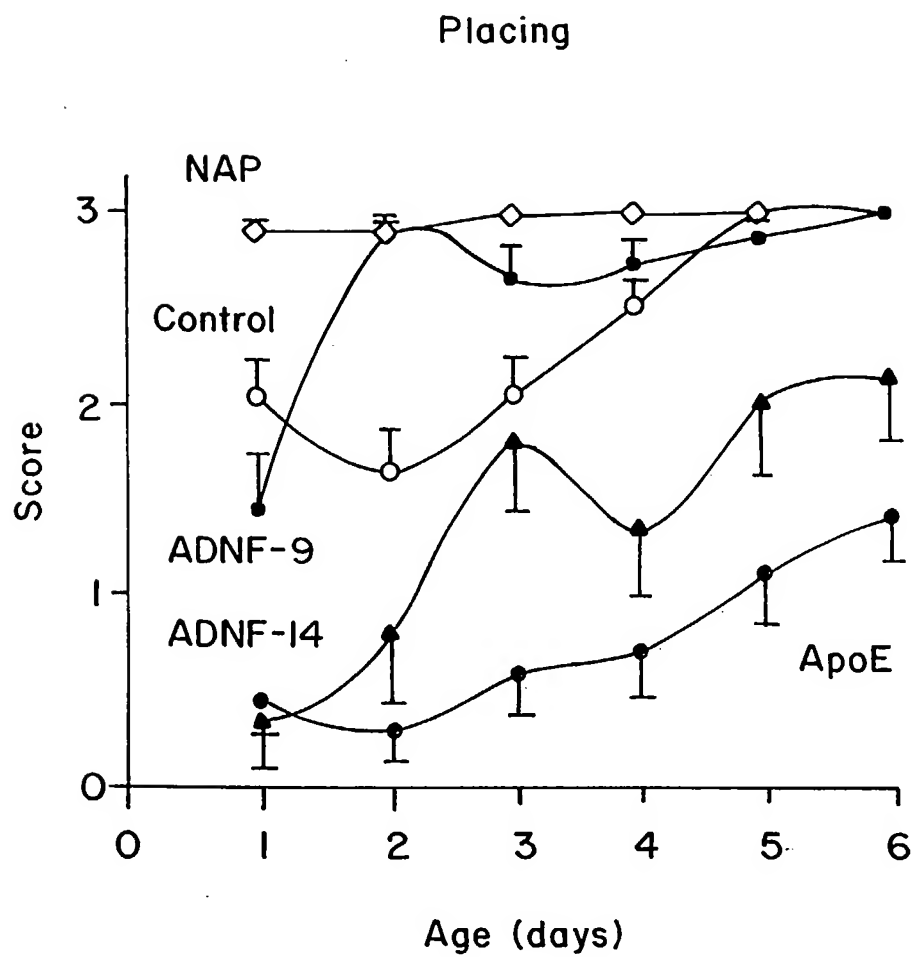


FIG. 17

Polymorphism

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H6 clone	GAGTTAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTC	CCTGGCATTG
H10 clone	GAGTTAACT	GANCANCCAN	CAGGCCTAAG	TGCCAGGTTN	CCTGGCGTTG
H3 clone	GAGTTAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTC	CCTGGCGTTG
H12 clone	GAGTTAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTC	CCTGGCGTTG
H7 clone	GAGTTAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTC	CCTGGCATTG
H4 clone	GAGTTAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTC	CCTGGCGTTG
H2 clone	GAGTTAACT	GAGCAGCCAA	CAGGCCTAAG	TGCCAGGTC	CCTGGCATTG

Polymorphic site: A → G transition

**FIG. 18.**